

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

WHAT IS CLAIMED IS:

1. A method for detecting the fungus *Stachybotrys chartarum*, comprising:  
 isolating DNA from a sample suspected of containing the fungus *Stachybotrys chartarum*;  
 subjecting the DNA to polymerase chain reaction amplification utilizing at least one primer, wherein the at least one primer comprises one of a (SEQ. ID NO. 1) 5'GTTGCTTCGGCGGGAAC3', (SEQ. ID NO. 2) 5'TTGCGTTTGCCACTCAGAG3', (SEQ. ID NO. 3) 5'ACCTATCGTTGCTTCGGCG3', and (SEQ. ID NO. 4) 5'GCGTTTGCCACTCAGAGAATACT3' base sequence; and  
 detecting the fungus *Stachybotrys chartarum* by visualizing the product of the polymerase chain reaction.
2. The method of claim 1, wherein subjecting the DNA to polymerase chain reaction further utilizes a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.
3. A primer set for detecting *Stachybotrys chartarum* using polymerase chain reaction, comprising:  
 a first primer comprising a base sequence (SEQ. ID NO. 1) 5'GTTGCTTCGGCGGGAAC3'; and  
 a second primer comprising a base sequence (SEQ. ID NO. 2) 5'TTGCGTTTGCCACTCAGAG3'.

4. The primer set of claim 3, wherein the first primer comprises a forward primer.
5. The primer set of claim 3, wherein the second primer comprises a reverse primer.
6. A primer set for detecting *Stachybotrys chartarum* using polymerase chain reaction, comprising:
  - a first primer comprising a first base sequence (SEQ. ID NO. 3)  
5'ACCTATCGTTGCTTCGGCG3'; and
  - a second primer comprising a second base sequence (SEQ. ID NO. 4)  
5'GCGTTTGCCACTCAGAGAATACT3'.
7. The primer set of claim 6, wherein the first primer comprises a forward primer.
8. The primer set of claim 6, wherein the second primer comprises a reverse primer.
9. A primer and probe set for detecting the fungus *Stachybotrys chartarum* using polymerase chain reaction, comprising:
  - a forward primer comprising a base sequence (SEQ. ID NO. 1)  
5'GTTGCTTCGGCGGGAAC3';
  - a reverse primer comprising a base sequence (SEQ. ID NO. 2)  
5'TTGCGTTTGCCACTCAGAG3'; and
  - a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-  
5'CTGCGCCCGGATCCAGGC3'-TAMRA.

10. A primer and probe set for detecting the fungus *Stachybotrys chartarum* using polymerase chain reaction, comprising:

a forward primer comprising a first base sequence (SEQ. ID NO. 3)

5'ACCTATCGTTGCTTCGGCG3';

a reverse primer comprising a second base sequence (SEQ. ID NO. 4)

5'GCGTTTGCCACTCAGAGAATACT3'; and

a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-

5'CTGCGCCCGGATCCAGGC3'-TAMRA.

11. A primer for use in polymerase chain reaction, comprising:

a base sequence comprising at least one of a first, second, third and fourth base sequence,

wherein the first base sequence comprises (SEQ. ID NO. 1)

5'GTTGCTTCGGCGGGAAC3',

wherein the second base sequence comprises (SEQ. ID NO. 2)

5'TTTGCGTTTGCCACTCAGAG3',

wherein the third base sequence comprises (SEQ. ID NO. 3)

5'ACCTATCGTTGCTTCGGCG3', and

wherein the fourth base sequence comprises (SEQ. ID NO. 4)

5'GCGTTTGCCACTCAGAGAATACT3'.

12. A method for detecting the presence of the fungus *Stachybotrys chartarum*, comprising:

obtaining a sample from the environment;

extracting DNA from the sample; and

amplifying the extracted DNA by polymerase chain reaction utilizing one or more primers to obtain an indication of the presence of *Stachybotrys chartarum* in the sample, wherein the one or more primers comprise at least one of a (SEQ. ID NO. 1) 5'GTTGCTTCGGCGGGAAC3', (SEQ. ID NO. 2) 5'TTGCGTTTGCCACTCAGAG3', (SEQ. ID NO. 3) 5'ACCTATCGTTGCTTCGGCG3', and (SEQ. ID NO. 4) 5'GCGTTTGCCACTCAGAGAATACT3' base sequence.

13. The method of claim 12, wherein amplifying the sample by polymerase chain reaction further utilizes a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.

14. A method for detecting the presence of the fungus *Stachybotrys chartarum*, comprising:

obtaining a sample from the environment;

extracting DNA from the sample; and

amplifying the extracted DNA by polymerase chain reaction utilizing a primer set to obtain an indication of the presence of *Stachybotrys chartarum* in the sample, wherein the primer set comprises:

a forward primer comprising a base sequence (SEQ. ID NO. 1)

5'GTTGCTTCGGCGGGAAC3', and

a reverse primer comprising a base sequence (SEQ. ID NO. 2)

5'TTGCGTTTGCCACTCAGAG3'.

15. The method of claim 14, wherein amplifying the sample by polymerase chain reaction further utilizes a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.

16. A method for detecting the presence of the fungus *Stachybotrys chartarum*, comprising:  
obtaining a sample from the environment;  
extracting DNA from the sample; and  
amplifying the extracted DNA by polymerase chain reaction utilizing a primer set to obtain an indication of the presence of *Stachybotrys chartarum* in the sample, wherein the primer set comprises:

a forward primer comprising a first base sequence (SEQ. ID NO. 3)

5'ACCTATCGTTGCTTCGGCG3', and

a reverse primer comprising a second base sequence (SEQ. ID NO. 4)

5'GCGTTTGCCACTCAGAGAATACT3'.

17. The method of claim 16, wherein amplifying the sample by polymerase chain reaction further utilizes a probe comprising a base sequence (SEQ. ID NO. 5) 6-FAM-5'CTGCGCCCGGATCCAGGC3'-TAMRA.

18. A method for identifying and quantifying the presence of the fungus *Stachybotrys chartarum* in a collected sample, comprising:

obtaining a primer set and probe that is specific for the fungal species *Stachybotrys chartarum*;

collecting the sample from the environment;

extracting the sample's DNA;

obtaining DNA standards from a culture of *Stachybotrys chartarum*;

determining the concentration of *Stachybotrys chartarum* spores in the DNA standards;

amplifying by polymerase chain reaction each of the DNA standards and the collected sample's DNA using the obtained primer set and probe; and

comparing amplification plots obtained by polymerase chain reaction of each of the DNA standards and the collected sample's DNA to obtain an indication of the presence of the fungus *Stachybotrys chartarum* in the collected sample and a concentration of the fungus *Stachybotrys chartarum* in the collected sample.